

# Untitled

ESULT 1

METK\_NEI MB

ID METK\_NEI MB

Reviewed;

389 AA.

AC Q9JY09;

DT 02-AUG-2002, integrated into UniProt KB/ Swiss-Prot.

DT 01-OCT-2000, sequence version 1.

DT 04-NOV-2008, entry version 50.

DE RecName: Full=S-adenosyl methionine synthetase;

DE EC=2.5.1.6;

DE AltName: Full=Methionine adenosyltransferase;

DE AltName: Full=AdoMet synthetase;

DE AltName: Full=MAT;

GN Name=metK; OrderedLocusNames=NMB1799;

OS Neisseria meningitidis serogroup B.

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

OC Neisseriaceae; Neisseria.

OX NCBI\_TaxID=491;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=MC58 / Serogroup B;

RX MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;

RA Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,

RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,

RA Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,

RA Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,

RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,

RA Cifton H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H.M.,

RA Qin H., Vamathevan J.J., Gill J., Scarlato V., Maignani V., Pizza M.,

RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,

RA Venter J.C.;

RT "Complete genome sequence of Neisseria meningitidis serogroup B strain

RT MC58.";

RL Science 287:1809-1815(2000).

CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from  
methionine and ATP. The overall synthetic reaction is composed of  
two sequential steps, AdoMet formation and the subsequent  
tripolyphosphate hydrolysis which occurs prior to release of  
AdoMet from the enzyme (By similarity).

CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +  
diphosphate + S-adenosyl-L-methionine.

CC -!- COFACTOR: Binds 2 divalent ions per subunit. Magnesium or cobalt  
(By similarity).

CC -!- COFACTOR: Binds 1 potassium ion per subunit (By similarity).

CC -!- PATHWAY: Amino-acid biosynthesis; S-adenosyl-L-methionine  
biosynthesis; S-adenosyl-L-methionine from L-methionine: step 1/1.

CC -!- SUBUNIT: Homotetramer (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasm

CC -!- SIMILARITY: Belongs to the AdoMet synthetase family.

CC -----  
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CC -----

DR EMBL; AE002098; AAF42136.1; -, Genomic DNA.

DR PIR; D81042; D81042.

DR RefSeq; NP\_274796.1; -.

DR HSSP; P04384; 1MXB.

DR GenBank; 903300; -.

DR GenomeReviews; AE002098\_GR; NMB1799.

DR KEGG; nme:NMB1799; -.

DR NMPDR; fig|122586.1.peg.1730; -.

DR TrEMBL; NMB1799; -.

DR HOGENOM; Q9JY09; -.

DR BioCyc; NMEN122586:NMB\_1799-MCN; -.

Untitled

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DR  GO: GO: 0005737; C: cytoplasm; IEA: HAMAP.
DR  GO: GO: 0005524; F: ATP binding; IEA: HAMAP.
DR  GO: GO: 0050897; F: cobalt ion binding; IEA: UniProtKB-KW
DR  GO: GO: 0000287; F: magnesium ion binding; IEA: HAMAP.
DR  GO: GO: 0004478; F: methionine adenosyltransferase activity; IEA: HAMAP.
DR  GO: GO: 0030955; F: potassium ion binding; IEA: UniProtKB-KW
DR  GO: GO: 0006730; P: one-carbon compound metabolic process; IEA: HAMAP.
DR  HAMAP: MF_00086; -; 1.
DR  InterPro: IPR002133; S-AdoMet_synthetase.
DR  PANTHER: PTHR11964; S-AdoMet_synt; 1.
DR  Pfam: PF02773; S-AdoMet_synt_C; 1.
DR  Pfam: PF02772; S-AdoMet_synt_M; 1.
DR  Pfam: PF00438; S-AdoMet_synt_N; 1.
DR  PIRSF: PIRSF000497; MAT; 1.
DR  TIGRFAMs: TIGR01034; metK; 1.
DR  PROSITE: PS00376; ADCMET_SYNTHETASE_1; 1.
DR  PROSITE: PS00377; ADCMET_SYNTHETASE_2; 1.
PE  3: Inferred from homology;
KW  ATP-binding; Cobalt; Complete proteome; Cytoplasm; Magnesium
KW  Metal-binding; Nucleotide-binding; One-carbon metabolism; Potassium
KW  Transferase.
FT  CHAIN 1 389 S-adenosyl methionine synthetase.
FT /FTId=PRO_0000174560.
FT NP_BIND 264 271 ATP (Potential).
FT METAL 17 17 Magnesium (By similarity).
FT METAL 43 43 Potassium (By similarity).
FT METAL 268 268 Potassium (By similarity).
FT METAL 276 276 Magnesium (By similarity).
SQ SEQUENCE 389 AA; 42099 MW 18F4E98E56084FA7 CRC64;

Query Match 100.0% Score 2003; DB 1; Length 389;
Best Local Similarity 100.0% Pred. No. 4.7e-148;
Matches 389; Conservative 0; Msmatches 0; Indels 0; Gaps 0;

Qy 1 MSEYLFTSESVSEGH-PDKVADQVSDAI LDAI LAQDPKARVAAETLVNTGLCVLAGEI TTT 60
Db 1 MSEYLFTSESVSEGH-PDKVADQVSDAI LDAI LAQDPKARVAAETLVNTGLCVLAGEI TTT 60

Qy 61 AQVDYI KVARETI KRI GYNSSSELGF DANGCAVG VYYDQQSPDI AGGVNEGEGI DLNQGAG 120
Db 61 AQVDYI KVARETI KRI GYNSSSELGF DANGCAVG VYYDQQSPDI AGGVNEGEGI DLNQGAG 120

Qy 121 DQGLMFGYACDETPTLMPFAI YYSHRLMQRQSEL RKGRLPWL RPDACAQL TVVYDSETG 180
Db 121 DQGLMFGYACDETPTLMPFAI YYSHRLMQRQSEL RKGRLPWL RPDACAQL TVVYDSETG 180

Qy 181 KVKRI DTVVLSTQHDPSTI AYEELKNAVI EHI I KPVLPSELLTDET KYLI NPTGRFVI GGP 240
Db 181 KVKRI DTVVLSTQHDPSTI AYEELKNAVI EHI I KPVLPSELLTDET KYLI NPTGRFVI GGP 240

Qy 241 QGDOGLTGRKI I VDTYGGAAPHGGGAFSGKDPSKVDRSAAYACRYVAKNI VAAGLATQQQ 300
Db 241 QGDOGLTGRKI I VDTYGGAAPHGGGAFSGKDPSKVDRSAAYACRYVAKNI VAAGLATQQQ 300

Qy 301 IQVSYAI GVAEPTSI SI DTFGTGKI SEEKLI ALVREHFDLRPKGI VQMLDLLRPI YSKSA 360
Db 301 IQVSYAI GVAEPTSI SI DTFGTGKI SEEKLI ALVREHFDLRPKGI VQMLDLLRPI YSKSA 360

Qy 361 AYG-HFGREEPEFTWERTDKAAALRAAAGL 389
Db 361 AYG-HFGREEPEFTWERTDKAAALRAAAGL 389

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